

Table S1. Tract lengths and number of SNPs for each conversion event subset studied.

Figure/Table reference	Subset	Median tract length (bp)	Mean (Median) number of SNPs in the tract
Table 1	All	906	9.5 (6)
	Simple	752.5	14.2 (5)
	Complex	1,948	8.8 (9.5)
Table S2	All	1,813	15.1 (12)
	Simple	1,740	16.8 (12)
	Complex	2,249	14.8 (12)
Figure 2	All	869.5	9.5 (6)
	CO	926	9.7 (6)
	NCO	790.5	9.3 (5)
Figure S1	All	145	4.2 (2)
	CO	134	4.3 (2)
	NCO	158	4.1 (2)
Figure 3	CO	1,017	9.8 (6)
	NCO	726.5	8.9 (5)
	CO; $\Delta GC > 0$	204	6.5 (2)
	CO; $\Delta GC \leq 0$	1,878	15.0 (12)
Table 2	All	1,471	12.9 (10)
	Flanking SNPs only	1,497	12.8 (10)
	Flanking SNPs excluded	1,564	13.2 (10)
Table S3	All	1,825	15.3 (12)
	Flanking SNPs only	1,834	15.0 (12)
	Flanking SNPs excluded	1,864	15.2 (12)

This table indicates the median length of conversion tracts (see below) and the mean (and median) number of SNPs in the conversion tract for each subset analysed in the study. The tract length is defined as the physical distance in base pairs (bp) between the two most distal SNPs within the tract.

Table S2. Conversion bias towards GC-bases for AT/GC SNPs involved in a recombination event (conversion tracts with at least 5 SNPs).

Conversion tract type	Number of genotyped SNP sites with AT/GC polymorphism^a	Conversion bias towards GC-bases (<i>b</i>)	P-value^b
All	70,374	0.013	< 0.001
Simple	57,897	0.013	0.0014
Complex	12,477	0.011	<i>N.S.</i>

^aThe conversion bias towards GC alleles (*b*) was computed for SNP sites located in conversion tracts containing at least 5 SNPs, taken all together or separating sites found in simple and complex conversion tracts.

^bone-sample proportion test, see methods, *N.S.*: non-significant.

Table S3. Conversion bias towards GC-richer haplotypes among AT_f/GC_f-polymorphism, considering all SNPs, or only flanking or internal SNPs (conversion tracts with at least 5 SNPs).

SNPs considered to classify haplotypes as AT- or GC-richer	Number of genotyped haplotypes with AT/GC-richer polymorphism^a	Conversion bias towards GC-richer haplotypes (<i>b</i>)	P-value^b
All	890	0.052	0.13
Flanking SNPs only	1,006	0.101	0.001
Flanking SNPs excluded	888	0.018	0.61

^aThe conversion bias towards GC-richer haplotypes (*b*) was computed for AT_f/GC_f polymorphisms located in CO-associated simple conversion tracts overlapping at least 5 SNPs. Haplotypes were categorized in AT- or GC-richer according to their difference in GC-content, considering all SNPs in the tract or only the two flanking SNPs or only the SNPs that are not the two flanking SNPs.

^bone-sample proportion test, see methods.

Table S4. Relative abundance of conversion tracts types, as predicted by the model of GC-biased MMR.

Case #	Parental haplotypes	Conversion tract	Relative abundance	Tract length
1	N...W N...S	N...W	$p_w x$	L_2
2	W...W S...S	W...W	$p_w (1-x)$	L_1
3	N...W N...S	N...S	$p_S x$	L_2
4	S...S W...W	S...S	$p_S (1-x)$	L_1
5	N...N N...N	N...N	$(2 - p_S - p_w) x$	L_1

For each of the five different types of conversion tracts produced after the repair of mismatches in heteroduplexes in crossover products (see Figure 4), we show the identity of the flanking bases observed in parental haplotypes (second column; S = G or C, W = A or T, N = Any base) and in the conversion tract (third column). The relative abundance in the gamete pool (fourth column) and the tract length (fifth column) are shown using parameters defined in Supplementary Text S3.

Table S5. Relative abundance of conversion tracts types among AT_f/GC_f-polymorphism, as predicted by the model of GC-biased MMR.

Case #	Parental haplotypes	Conversion tract	Relative tract abundance	Tract length
1	W...W S...S	W...W	$r p_w x$	L_2
2	W...W S...S	W...W	$p_w (1-x)$	L_1
3	W...W S...S	S...S	$r p_s x$	L_2
4	S...S W...W	S...S	$p_s (1-x)$	L_1
5	W...W S...S	W...W	$r^2 (2 - p_s - p_w) x$	L_1
5	S...S W...W	S...S	$r^2 (2 - p_s - p_w) x$	L_1

For each of the five different types of conversion tracts produced after the repair of mismatches in heteroduplexes in crossover products among the subset of AT_f/GC_f-polymorphism, we show the identity of the flanking bases observed in parental haplotypes (second column; S = G or C, W = A or T, N = Any base) and in the conversion tract (third column). The relative abundance in the gamete pool (fourth column) and the tract length (fifth column) are shown using parameters described in Supplementary Text S3.